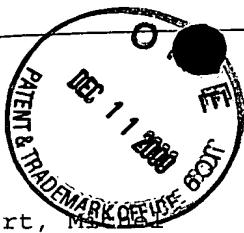


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SEQUENCE LISTING



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National Research Council of Canada

TECH CENTER 1600/2000

<120> Fusion Proteins for Use in Enzymatic Synthesis of Oligosaccharides

<130> 019957-012910US

<140> US 09/211,691

<141> 1998-12-14

<150> US 60/069,443

<151> 1997-12-15

<160> 18

<170> PatentIn Ver. 2.1

<210> 1

<211> 828

<212> DNA

<213> Neisseria meningitidis

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<223> beta-1,4-galactosyltransferase (lgtB)

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Met Gln Asn His Val Ile Ser Leu Ala Ser Ala Ala Glu Arg Arg Ala
1 5 10 15

48

cac att gcc gat acc ttc ggc agg cac ggc atc ccg ttt cag ttt ttc
His Ile Ala Asp Thr Phe Gly Arg His Gly Ile Pro Phe Gln Phe Phe
20 25 30

96

gac gca ctg atg ccg tct gaa agg ctg gaa cag gca atg gcg gaa ctc
Asp Ala Leu Met Pro Ser Glu Arg Leu Glu Gln Ala Met Ala Glu Leu
35 40 45

144

gtc ccc ggc ttg tcg gcg cac ccc tat ttg agc gga gtg gaa aaa gcc
Val Pro Gly Leu Ser Ala His Pro Tyr Leu Ser Gly Val Glu Lys Ala
50 55 60

192

tgc ttt atg agc cac gcc gta ttg tgg aag cag gca ttg gac gaa ggt
Cys Phe Met Ser His Ala Val Leu Trp Lys Gln Ala Leu Asp Glu Gly
65 70 75 80

240

ctg ccg tat atc acc gta ttt gag gac gac gtt tta ctc ggc gaa ggt
Leu Pro Tyr Ile Thr Val Phe Glu Asp Asp Val Leu Leu Gly Glu Gly
85 90 95

288

gag gaa aaa ttc ctt gcc gaa gac gct tgg ctg caa gaa cgc ttt gac
Glu Glu Lys Phe Leu Ala Glu Asp Ala Trp Leu Gln Glu Arg Phe Asp
100 105 110

336

ccg gat acc gcc ttt atc gtc cgc ttg gaa acg atg ttt atg cac gtc Pro Asp Thr Ala Phe Ile Val Arg Leu Glu Thr Met Phe Met His Val 115 120 125	384
ctg acc tcg ccc tcc ggc gtg gcg gat tac tgc ggg cgc gcc ttt ccg Leu Thr Ser Pro Ser Gly Val Ala Asp Tyr Cys Gly Arg Ala Phe Pro 130 135 140	432
ctg ttg gaa agc gaa cac tgg ggg acg gcg ggc tat atc att tcc cga Leu Leu Glu Ser Glu His Trp Gly Thr Ala Gly Tyr Ile Ile Ser Arg 145 150 155 160	480
aaa gcg atg cgg ttt ttc ctg gac agg ttt gcc gcc ctg ccg ccc gaa Lys Ala Met Arg Phe Phe Leu Asp Arg Phe Ala Ala Leu Pro Pro Glu 165 170 175	528
ggg ctg cac ccc gtc gat ctg atg atg ttc agc gat ttt ttc gac agg Gly Leu His Pro Val Asp Leu Met Met Phe Ser Asp Phe Phe Asp Arg 180 185 190	576
gaa gga atg ccg gtt tgc cag ctc aat ccc gcc ttg tgc gcc caa gag Glu Gly Met Pro Val Cys Gln Leu Asn Pro Ala Leu Cys Ala Gln Glu 195 200 205	624
ctg cat tat gcc aag ttt cac gac caa aac agc gca ttg ggc agc ctg Leu His Tyr Ala Lys Phe His Asp Gln Asn Ser Ala Leu Gly Ser Leu 210 215 220	672
atc gaa cac gac cgc ctc ctg aac cgc aaa cag caa agg cgc gat tcc Ile Glu His Asp Arg Leu Leu Asn Arg Lys Gln Gln Arg Arg Asp Ser 225 230 235 240	720
ccc gcc aac aca ttc aaa cac cgc ctg. atc cgc gcc ttg acc aaa atc Pro Ala Asn Thr Phe Lys His Arg Leu Ile Arg Ala Leu Thr Lys Ile 245 250 255	768
agc agg gaa agg gaa aaa cgc cgg caa agg cgc gaa cag ttc att gtg Ser Arg Glu Arg Glu Lys Arg Arg Gln Arg Arg Glu Gln Phe Ile Val 260 265 270	816
cct ttc caa taa Pro Phe Gln 275	828
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His Ile Ala Asp Thr Phe Gly Arg His Gly Ile Pro Phe Gln Phe Phe 20 25 30	
Asp Ala Leu Met Pro Ser Glu Arg Leu Glu Gln Ala Met Ala Glu Leu 35 40 45	
Val Pro Gly Leu Ser Ala His Pro Tyr Leu Ser Gly Val Glu Lys Ala 50 55 60	
Cys Phe Met Ser His Ala Val Leu Trp Lys Gln Ala Leu Asp Glu Gly 65 70 75 80	

Leu Pro Tyr Ile Thr Val Phe Glu Asp Asp Val Leu Leu Gly Glu Gly
 85 90 95
 Glu Glu Lys Phe Leu Ala Glu Asp Ala Trp Leu Gln Glu Arg Phe Asp
 100 105 110
 Pro Asp Thr Ala Phe Ile Val Arg Leu Glu Thr Met Phe Met His Val
 115 120 125
 Leu Thr Ser Pro Ser Gly Val Ala Asp Tyr Cys Gly Arg Ala Phe Pro
 130 135 140
 Leu Leu Glu Ser Glu His Trp Gly Thr Ala Gly Tyr Ile Ile Ser Arg
 145 150 155 160
 Lys Ala Met Arg Phe Phe Leu Asp Arg Phe Ala Ala Leu Pro Pro Glu
 165 170 175
 Gly Leu His Pro Val Asp Leu Met Met Phe Ser Asp Phe Phe Asp Arg
 180 185 190
 Glu Gly Met Pro Val Cys Gln Leu Asn Pro Ala Leu Cys Ala Gln Glu
 195 200 205
 Leu His Tyr Ala Lys Phe His Asp Gln Asn Ser Ala Leu Gly Ser Leu
 210 215 220
 Ile Glu His Asp Arg Leu Leu Asn Arg Lys Gln Gln Arg Arg Asp Ser
 225 230 235 240
 Pro Ala Asn Thr Phe Lys His Arg Leu Ile Arg Ala Leu Thr Lys Ile
 245 250 255
 Ser Arg Glu Arg Glu Lys Arg Arg Gln Arg Arg Glu Gln Phe Ile Val
 260 265 270
 Pro Phe Gln
 275

<210> 3
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 primer

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^{cont}
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37

<210> 6
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
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<210> 7
<211> 9
<212> PRT
<213> Artificial Sequence

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<210> 8
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<210> 9
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<212> DNA
<213> Artificial Sequence

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<211> 42
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<210> 11
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<210> 12
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<210> 14
<211> 6
<212> PRT
<213> Artificial Sequence

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<223> Description of Artificial Sequence:6-His tail for
      purification

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<400> 14
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<210> 15
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 15
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<210> 16
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 Pro Lys Gly Tyr Asp Asp Arg Gly Gly Ala Ser Val Gln Asn His
 1 5 10 15

gtt atc agc tta gct 63
 Val Ile Ser Leu Ala
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a²
Cont
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 <211> 21
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 of the galE-lgtB fusion

<400> 17
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 1 5 10 15
 Val Ile Ser Leu Ala
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<210> 18
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 <212> PRT
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<223> Description of Artificial Sequence:peptide linker

a²
Cont

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Gly Gly Gly Ile
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